

09/373984

```
=> s low temperature(10a)PCR
L1          23 LOW TEMPERATURE(10A) PCR

=> s l1 and (exten#### (10a)degree)
L2          0 L1 AND (EXTEN#### (10A) DEGREE)

=> s l1 and temperature#
L3          23 L1 AND TEMPERATURE#

=> s l3 and (inactivat###(10a)polymerase#)
L4          0 L3 AND (INACTIVAT###(10A) POLYMERASE#)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L5          15 DUP REM L3 (8 DUPLICATES REMOVED)

=> d l5 1-15 bib ab kwic

L5  ANSWER 1 OF 15  CAPLUS  COPYRIGHT 2004 ACS on STN
AN  2003:691259  CAPLUS
DN  139:319964
TI  Study of microorganism viability and integrity of structural sites of
    their DNA, amplified in PCR after low-
    temperature storage under different conditions
AU  Vysekantsev, I. P.; Omelchenko, E. A.; Gurina, T. M.
CS  Institute for Problems of Cryobiology and Cryomedicine, National Academy
    of Sciences of the Ukraine, Kharkov, Ukraine
SO  Problemy Kriobiologii (2003), (1), 71-75
    CODEN: PKRIEA; ISSN: 1026-1230
PB  Institut Problem Kriobiologii i Kriomedititsiny NAN Ukrainy
DT  Journal
LA  Russian/English
AB  The obtained exptl. data testify to the fact that under low temperature
    preservation the cyclic changes in storage temperature from -196 to
    -100°C can result in addnl. death of microbial cells. In microbial
    cells, stored under liquid nitrogen constant temperature and under conditions
of  storage temperature variation within the mentioned range, the DNA structural
    sites are preserved, providing the amplification in polymerase chain
    reaction (PCR) of specific fragments.
TI  Study of microorganism viability and integrity of structural sites of
    their DNA, amplified in PCR after low-
    temperature storage under different conditions

L5  ANSWER 2 OF 15  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN  2003:544635  BIOSIS
DN  PREV200300546248
TI  Photobacterium profundum strain SS9: Model organism for low-
    temperature and high-pressure functional genomics studies.
AU  Lauro, F. M. [Reprint Author]; Tran, K. [Reprint Author]; Phillips, Y. M.
    [Reprint Author]; Takami, H.; Vezzi, A.; Valle, G.; Bartlett, D. H.
    [Reprint Author]
CS  University of California San Diego, La Jolla, CA, USA
SO  Abstracts of the General Meeting of the American Society for Microbiology,
    (2003) Vol. 103, pp. N-336. http://www.asmtusa.org/mtgsrc/generalmeeting.htm.
    m. cd-rom.
    Meeting Info.: 103rd American Society for Microbiology General Meeting.
    Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
    ISSN: 1060-2011 (ISSN print).
DT  Conference; (Meeting)
    Conference; Abstract; (Meeting Abstract)
LA  English
ED  Entered STN: 19 Nov 2003
    Last Updated on STN: 19 Nov 2003
```

AB The deep-sea benthos is generally characterized as an environment of low **temperature**, high pressure, high proportions of recalcitrant organics and high invertebrate diversity. The bacterium *Photobacterium profundum* strain SS9 is being used as a model system for studying microbial adaptations to the above conditions. It is a psychrotolerant and moderately piezophilic isolate obtained from a deep-sea amphipod crustacean. It grows relatively rapidly and is amenable to a variety of genetic manipulations. In addition, this species appears to be widely distributed, having been isolated by several groups from a number of deep-sea western Pacific Ocean environmental samples. An SS9 genome project is currently in its final stages. To further examine SS9 gene function, transposon mutagenesis has been used to identify genes important for growth at low **temperature** or high pressure. Cold-sensitive (CS) mutants have been isolated by screening for transposon mutants unable to grow at 4degreeC. Pressure-sensitive (PS) mutants have been obtained by screening liquid cultures in 96-well PCR plates at 45 MPa. Both mini-Tn10 and hypertransposable mini-Tn5 transposons have been employed. Putative CS and PS mutants have been further evaluated in terms of growth lag, rate or culture density defects under non-permissive conditions. Genes responsible for low-**temperature** or high-pressure growth have been obtained by arbitrary PCR cloning and sequencing of DNA flanking the sites of Tn10 or Tn5. The sequences obtained have been searched through the unfinished SS9 genome to retrieve full length ORFs and possible downstream genes whose expression could be influenced by the transposon insertion. The mutated genes belong to various classes, including genes involved in chromosome partitioning and cell division, LPS biosynthesis, and genes encoding regulators of transcription, RNA stability and protein turnover. Complementation experiments are in progress to verify the identification of the CS and PS genes. The possible significance of the genes identified to bacterial life at low **temperature** or at high pressure will be discussed.

TI *Photobacterium profundum* strain SS9: Model organism for low-**temperature** and high-pressure functional genomics studies.

AB The deep-sea benthos is generally characterized as an environment of low **temperature**, high pressure, high proportions of recalcitrant organics and high invertebrate diversity. The bacterium *Photobacterium profundum* strain SS9 is being used. . . stages. To further examine SS9 gene function, transposon mutagenesis has been used to identify genes important for growth at low **temperature** or high pressure. Cold-sensitive (CS) mutants have been isolated by screening for transposon mutants unable to grow at 4degreeC. Pressure-sensitive. . . have been further evaluated in terms of growth lag, rate or culture density defects under non-permissive conditions. Genes responsible for low-**temperature** or high-pressure growth have been obtained by arbitrary PCR cloning and sequencing of DNA flanking the sites of Tn10 or Tn5. The sequences obtained have been searched through the. . . the identification of the CS and PS genes. The possible significance of the genes identified to bacterial life at low **temperature** or at high pressure will be discussed.

IT . . . laboratory techniques

IT Miscellaneous Descriptors  
bacterial genetics; bacterial physiology; cell division; environmental samples: analysis; extreme environments; functional genomics studies: high-pressure, low-**temperature**; gene expression; gene function; gene mutations; growth **temperature**; microbial ecology; open reading frames; pressure; **temperature**; transposons

L5 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2002:964473 CAPLUS

DN 138:34103

TI Kits for low **temperature** cycle extension of DNA with high priming specificity during PCR

IN Hong, Guo Fan; Yang, Yongjie; Zhu, Jia  
PA Shanghai Mendel DNA Center Co., Ltd, Peop. Rep. China  
SO PCT Int. Appl., 61 pp.  
CODEN: PIXXD2  
DT Patent  
LA English  
FAN.CNT 2

|      | PATENT NO.     | KIND   | DATE     | APPLICATION NO. | DATE     |
|------|----------------|--|----------|-----------------|----------|
| PI   | WO 2002101004  | A2   | 20021219 | WO 2002-IB3341  | 20020605 |
|      | W:             | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM |          |                 |          |
|      | RW:            | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG   |          |                 |          |
|      | US 2003087237  | A1   | 20030508 | US 2001-878131  | 20010608 |
| PRAI | US 2001-878131 | A  | 20010608 |                 |          |
|      | CN 2001-117603 | A  | 20010430 |                 |          |

AB The invention relates to methods for extending a primer or a pair of primers in low-temperature cycle DNA amplification for cycle sequencing and PCR.

In particular, the methods contemplate the combined use of moderately thermostable DNA polymerases in the presence of a low concentration of glycerol or ethylene glycol or the mixts. thereof, as an agent to reduce the melting temperature of DNA. Predistributed reaction mixts. of a high-fidelity and high processivity DNA polymerase stable at room temperature for several weeks in ready-to-use kits are also contemplated by the invention. In a preferred embodiment, the DNA polymerase is selected from *Bacillus caldolyticus*, *Bacillus caldotenax* or *Bacillus stearothermophilus*.

TI Kits for **low temperature** cycle extension of DNA with high priming specificity during PCR

IT Nucleic acid hybridization  
PCR (polymerase chain reaction)

**Temperature** effects, biological

Test kits

(kits for low temperature cycle extension of DNA with high priming specificity during PCR)

L5 ANSWER 4 OF 15 MEDLINE on STN DUPLICATE 1

AN 1999157106 MEDLINE

DN PubMed ID: 10037825

TI **Low temperature** cycled PCR protocol for  
Klenow fragment of DNA polymerase I in the presence of proline.

AU Iakobashvili R; Lapidot A

CS Department of Organic Chemistry, The Weizmann Institute of Science, Rehovot 76100, Israel.

SO Nucleic acids research, (1999 Mar 15) 27 (6) 1566-8.

Journal code: 0411011. ISSN: 0305-1048.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199904

ED Entered STN: 19990511

Last Updated on STN: 19990511

Entered Medline: 19990427

AB A method for performing cycled PCR at low **temperatures**, using the thermolabile Klenow fragment of DNA polymerase I, is reported. Application of proline as a buffer additive in the range of 3.0-5.5 M

remarkably increases the thermal stability of the polymerase and decreases the denaturation **temperature** of DNAtemplate. This method might be applicable to a broad spectrum of thermolabile DNA polymerases in cycled PCR and other methods of DNA amplification.

- TI Low **temperature** cycled PCR protocol for  
Klenow fragment of DNA polymerase I in the presence of proline.
- AB A method for performing cycled PCR at low **temperatures**, using  
the thermolabile Klenow fragment of DNA polymerase I, is reported.  
Application of proline as a buffer additive in the range of 3.0-5.5 M  
remarkably increases the thermal stability of the polymerase and decreases  
the denaturation **temperature** of DNAtemplate. This method might  
be applicable to a broad spectrum of thermolabile DNA polymerases in  
cycled PCR and other. . . .
- L5 ANSWER 5 OF 15 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1999:431667 BIOSIS  
DN PREV199900431667  
TI The barley (*Hordeum vulgare* L.) dehydrin multigene family: Sequences,  
allele types, chromosome assignments, and expression characteristics of 11  
Dhn genes of cv Dicktoo.
- AU Choi, D.-W.; Zhu, B.; Close, T. J. [Reprint author]  
CS Department of Botany and Plant Sciences, University of California,  
Riverside, CA, 92521-0124, USA  
SO Theoretical and Applied Genetics, (June, 1999) Vol. 98, No. 8, pp.  
1234-1247. print.  
CODEN: THAGA6. ISSN: 0040-5752.
- DT Article  
LA English  
ED Entered STN: 18 Oct 1999  
Last Updated on STN: 18 Oct 1999
- AB Dehydrins (LEA D11 proteins) have been identified in both higher and lower  
plants, and are associated with tolerance to, or response to the onset of,  
low **temperature** or dehydration. Several studies have suggested  
that specific alleles of Dhn genes may contribute to a number of  
phenotypic traits, including the emergence of seedlings in cool or saline  
soils and the frost tolerance of more-mature plants. However, an  
incomplete collection of the Dhn multigene family in any system and  
nucleic acid cross-hybridization between Dhn gene-family members have  
limited the precision of these studies. We attempted to overcome these  
impediments by determining the nucleotide sequences of the entire Dhn  
multigene family in barley and by developing gene-specific probes. We  
identified 11 unique Dicktoo Dhn genes. Seven appear to be alleles of Dhn  
genes identified previously in other barley cultivars. Another, Dhn9,  
appears to be orthologous to a *Triticum durum* Dhn gene. A statistical  
analysis of the total collection of genomic clones brings the estimated  
size of the barley Dhn gene family to 13. Allelic differences in the  
protein-coding regions appear to result principally from duplications of  
entire PHI-segments or single amino-acid substitutions, suggesting that  
poly-peptide structural constraints have been a strong force in the  
evolution of Dhn alleles. Chromosome mapping by PCR with wheat-barley  
addition lines established the presence of Dhn genes in four barley  
chromosomes (3H, 4H, 5H, 6H). RT-PCR demonstrated that the Dhn  
genes are differentially regulated under dehydration, low  
**temperature** and ABA treatment, consistent with putative regulatory  
elements located upstream of the respective Dhn coding regions. This  
whole-genome, gene-specific study unifies what previously seemed to be  
disparate-mapping, expression, and genetic-variation data for Dhn genes in  
the Triticeae and other plant systems.
- AB. . . identified in both higher and lower plants, and are associated with  
tolerance to, or response to the onset of, low **temperature** or  
dehydration. Several studies have suggested that specific alleles of Dhn  
genes may contribute to a number of phenotypic traits, . . . by PCR with  
wheat-barley addition lines established the presence of Dhn genes in four  
barley chromosomes (3H, 4H, 5H, 6H). RT-PCR demonstrated that

the Dhn genes are differentially regulated under dehydration, **low temperature** and ABA treatment, consistent with putative regulatory elements located upstream of the respective Dhn coding regions. This whole-genome, gene-specific study. . .

L5 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2000:163266 CAPLUS  
DN 133:203465  
TI Sex determination from human tissues by modified formamide **low temperature** (FoLT)-PCR method  
AU Yasuda, Seiji; Kimura, Akihiko; Inoue, Hiroshi; Fujii, Toshihiro; Kawasaki, Keishi; Sonobe, Akifumi; Tsuji, Tsutomu  
CS Department of Forensic Medicine, Wakayama Medical College, Japan  
SO DNA Takei (1998), 6, 192-197  
CODEN: DNTAFM  
PB Toyo Shoten  
DT Journal  
LA Japanese  
AB With 4 DNA primers based on the amelogenin gene and the SRY gene, the modified formamide low temperature (FoLT)-PCR method was effective for sex determination  
of human tissues such as brain, lung, heart, liver, skin, muscle, etc. In this modified method, the tissue sample was treated with formamide at 95° and 72° before the PCR anal.  
TI Sex determination from human tissues by modified formamide **low temperature** (FoLT)-PCR method

L5 ANSWER 7 OF 15 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN  
AN 1998384172 EMBASE  
TI Rapid discrimination of psychrotolerant and mesophilic strains of the Bacillus cereus group by PCR targeting of 16S rDNA.  
AU Von Stetten F.; Francis K.P.; Lechner S.; Neuhaus K.; Scherer S.  
CS S. Scherer, Institut für Mikrobiologie, Forschungszentrum Milch/Lebensmittel, Technische Universität München, Weißenstephaner Berg 3, D-85350 Freising-Weißenstephan, Germany. 100424.2340@compuserve.com  
SO Journal of Microbiological Methods, (1998) 34/2 (99-106).  
Refs: 27  
ISSN: 0167-7012 CODEN: JMIMDQ  
PUI S 0167-7012(98)00077-3  
CY Netherlands  
DT Journal; Article  
FS 004 Microbiology  
LA English  
SL English  
AB The paper describes a novel PCR assay for discriminating psychrotolerant and mesophilic strains of the Bacillus cereus group by targeting of 16S rDNA signatures. Application of the assay circumvents long-term growth tests at **low temperature** currently used to detect psychrotolerant strains. PCR was performed with pure cultures. A 100% correlation of PCR and growth data at 7°C was obtained for the 194 B. cereus group strains tested. Potential applications of the assay for the dairy industry and agriculture are suggested. Copyright (C) 1998 Elsevier Science B.V.  
AB . . . of the Bacillus cereus group by targeting of 16S rDNA signatures. Application of the assay circumvents long-term growth tests at **low temperature** currently used to detect psychrotolerant strains. PCR was performed with pure cultures. A 100% correlation of PCR and growth data at 7°C was obtained for the 194. . .  
CT Medical Descriptors:  
\*bacillus cereus  
\*temperature sensitivity  
polymerase chain reaction  
assay

bacterial growth  
nonhuman  
article  
priority journal  
\*ribosome DNA: EC, endogenous compound  
RNA 16s  
bacterial DNA: EC, endogenous compound

L5 ANSWER 8 OF 15 MEDLINE on STN DUPLICATE 2  
AN 96178871 MEDLINE  
DN PubMed ID: 8616256  
TI Induction of homologous low **temperature** and ABA-responsive genes  
in frost resistant (*Solanum commersonii*) and frost-sensitive (*Solanum*  
*tuberosum* cv. Bintje) potato species.  
AU Baudo M M; Meza-Zepeda L A; Palva E T; Heino P  
CS Department of Molecular Genetics, Uppsala Genetic Center, Swedish  
University of Agricultural Sciences, Uppsala, Sweden.  
SO Plant molecular biology, (1996 Jan) 30 (2) 331-6.  
Journal code: 9106343. ISSN: 0167-4412.  
CY Netherlands  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals  
OS GENBANK-X83596; GENBANK-X83597  
EM 199606  
ED Entered STN: 19960620  
Last Updated on STN: 19970203  
Entered Medline: 19960612  
AB A DNA fragment corresponding to a **low-temperature**- and  
ABA-responsive gene (*Scdhn1*) was amplified by **PCR** from genomic  
DNA of a wild, frost-resistant potato species, *Solanum commersonii*. A  
homologous gene (*Stdhn1*) was identified in *Solanum tuberosum* cv. Bintje,  
a frost-sensitive domesticated potato cultivar. The expression of the  
gene was studied during low **temperature** and ABA treatments in  
both *Solanum* species. The analysis revealed that both low  
**temperature** and ABA lead to the accumulation of a 1 kb transcript  
that corresponded to the PCR fragment. The induction of the gene was  
relatively rapid and maximum amounts of the transcripts were detected  
already after 1 day and 7 h of treatment with low **temperature**  
and ABA, respectively. Previous results have shown that there is no  
increase in the amount of endogenous ABA in *S. tuberosum* during low-  
**temperature** treatment, which indicates that two independent  
signalling pathways lead to the induction of this gene.  
TI Induction of homologous low **temperature** and ABA-responsive genes  
in frost resistant (*Solanum commersonii*) and frost-sensitive (*Solanum*  
*tuberosum* cv. Bintje) potato species.  
AB A DNA fragment corresponding to a **low-temperature**- and  
ABA-responsive gene (*Scdhn1*) was amplified by **PCR** from genomic  
DNA of a wild, frost-resistant potato species, *Solanum commersonii*. A  
homologous gene (*Stdhn1*) was identified in *Solanum tuberosum* cv. Bintje,  
a frost-sensitive domesticated potato cultivar. The expression of the  
gene was studied during low **temperature** and ABA treatments in  
both *Solanum* species. The analysis revealed that both low  
**temperature** and ABA lead to the accumulation of a 1 kb transcript  
that corresponded to the PCR fragment. The induction of. . . rapid and  
maximum amounts of the transcripts were detected already after 1 day and 7  
h of treatment with low **temperature** and ABA, respectively.  
Previous results have shown that there is no increase in the amount of  
endogenous ABA in *S. tuberosum* during low-**temperature** treatment,  
which indicates that two independent signalling pathways lead to the  
induction of this gene.  
L5 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 1995:615953 CAPLUS

DN 123:134107  
 TI Formamide **low-temperature PCR**: applications  
 for direct PCR from clinical material  
 AU Panaccio, Michael; French, Michelle; Lew, Andrew  
 CS Dep. Mol. Biol., Victorian Inst. Animal Sc., Attwood, Australia  
 SO Methods in Neurosciences (1995), 26, 3-14  
 CODEN: MENE5; ISSN: 1043-9471  
 DT Journal  
 LA English  
 AB Formamide low-temperature (FoLT) PCR is a rapid PCR protocol that was designed to allow direct PCR amplification from whole blood. A slight modification of the pre-cycling procedure allows FoLT PCR to be reproducibly applied to solid tissue samples. However, FoLT PCR is not recommended for use in samples that may contain mucus. One of the advantages of FoLT PCR is that it is suitable for use with most widely used anticoagulants. Another advantage is that it is well suited for studies involving the transportation of samples. The use of FoLT PCR has been demonstrated in genetic screening directly from blood samples, screening transgenic mice, and mapping intron-exon boundaries directly from solid tissues.  
 TI Formamide **low-temperature PCR**: applications  
 for direct PCR from clinical material

L5 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:642954 CAPLUS  
 DN 119:242954  
 TI DNA amplification by polymerase chain reaction (PCR) under  
**low temperature**  
 IN Nishimura, Naoyuki  
 PA Shimadzu Corp, Japan  
 SO Jpn. Kokai Tokkyo Koho, 10 pp.  
 CODEN: JKXXAF  
 DT Patent  
 LA Japanese  
 FAN.CNT 1

|      | PATENT NO.     | KIND | DATE     | APPLICATION NO. | DATE     |
|------|----------------|------|----------|-----------------|----------|
| PI   | JP 05244950    | A2   | 19930924 | JP 1992-189980  | 19920623 |
|      | JP 2576741     | B2   | 19970129 |                 |          |
| PRAI | JP 1991-262956 |      | 19910912 |                 |          |

AB DNA of interest is amplified by PCR at  $\leq 25^\circ$ , preferably at  $\leq 15^\circ$ . The method increases the efficiency of PCR and reduces the side-reactions between the primers and between the primer and DNA template which contains sequences similar to the primer. Moreover, the low-temperature PCR is useful for quantification of the DNA of interest.  
 TI DNA amplification by polymerase chain reaction (PCR) under  
**low temperature**  
 IT **Temperature**  
 (low, amplification of DNA by PCR at)

L5 ANSWER 11 OF 15 MEDLINE on STN  
 AN 94003822 MEDLINE  
 DN PubMed ID: 8400703  
 TI The use of RAPDs for the analysis of parasites.  
 AU Simpson A J; Dias Neto E; Steindel M; Caballero O L; Passos L K; Pena S D  
 CS Laboratorio de Bioquimica e Biologia Molecular, Centro de Pesquisas Rene Rachou, Belo Horizonte, Minas Gerais, Brazil.  
 SO EXS, (1993) 67 331-7.  
 Journal code: 9204529.  
 CY Switzerland  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 199311  
 ED Entered STN: 19940117

Last Updated on STN: 19980206

Entered Medline: 19931105

AB There is a lack of sequence information concerning polymorphic loci in parasite genomes. Thus, the use of arbitrary **PCR** primers under **low temperature** annealing conditions to generate random amplified polymorphic DNAs (RAPDs) represents an important approach to the study of the structure of parasite populations, their genetic variation as well as improved diagnosis of the diseases they cause. Following the examination of all variables and their effect on the reproducibility of the reaction, we have established a protocol for the analysis of RAPDs that involves amplification at two separate DNA concentrations followed by polyacrylamide gel electrophoresis and silver staining. We find the technique to be sensitive, reproducible, simple and relatively cheap. It has already provided insight into the genetic variation in populations of schistosomes and trypanosomes and is being used to study various other endemic infections. We also use specific primers under low stringency conditions in situations where the objective of the amplification is the detection of a particular sequence and where normal high stringency conditions give a positive/negative answer such as sex determination or diagnosis of blood born infections. Under low stringency conditions, specific amplification products persist but products of low stringency priming are also apparent and serve as a perfect internal control for negative samples.

AB There is a lack of sequence information concerning polymorphic loci in parasite genomes. Thus, the use of arbitrary **PCR** primers under **low temperature** annealing conditions to generate random amplified polymorphic DNAs (RAPDs) represents an important approach to the study of the structure of. . .

L5 ANSWER 12 OF 15 MEDLINE on STN

DUPLICATE 3

AN 93159785 MEDLINE

DN PubMed ID: 8431290

TI FoLT PCR: a simple PCR protocol for amplifying DNA directly from whole blood.

AU Panaccio M; Georgesz M; Lew A M

CS Victorian Institute of Animal Sciences, Australia.

SO BioTechniques, (1993 Feb) 14 (2) 238-43.

Journal code: 8306785. ISSN: 0736-6205.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199303

ED Entered STN: 19930402

Last Updated on STN: 19930402

Entered Medline: 19930315

AB FoLT (formamide **low temperature**) **PCR** is a protocol for amplifying DNA directly from whole blood without any preparative steps. Up to 10% (vol/vol) whole blood can be added directly into the tube containing the PCR mixture. There is no need for transfers, centrifugations, pre-boiling or any preparative step. It involves the use of formamide (18% vol/vol) as well as reduced incubation **temperatures** (cycles of 85 degrees, 40 degrees, 60 degrees C). The type of anticoagulant used was critical: sodium heparin or EDTA being superior to lithium or fluoride heparin. Our studies indicate that FoLT PCR probably works by reducing the amount of protein coagulation and allowing more DNA template to be accessible for amplification. The sensitivity of FoLT PCR is such that a single copy gene from 5.5 nucleated cells in 1 microliter of whole blood can be detected.

AB FoLT (formamide **low temperature**) **PCR** is a protocol for amplifying DNA directly from whole blood without any preparative steps. Up to 10% (vol/vol) whole blood. . . transfers, centrifugations, pre-boiling or any preparative step. It involves the use of formamide (18% vol/vol) as well as reduced incubation



**temperatures** (cycles of 85 degrees, 40 degrees, 60 degrees C).  
The type of anticoagulant used was critical: sodium heparin or EDTA. . .

CT

genetics

DNA, Bacterial: GE, genetics  
Edetic Acid  
\*Formamides  
Heparin  
Indicators and Reagents  
Molecular Sequence Data  
\*Polymerase Chain Reaction: MT, methods  
**Temperature**

L5 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1991:140034 CAPLUS

DN 114:140034

TI **Low temperature** effect on **PCR** and  
chlorophyll accumulation in rye seedlings

AU Krol, M.; Huner, N. P. A.

CS Dep. Plant Sci., Univ. West. Ontario, London, ON, N6A 5B7, Can.

SO Curr. Res. Photosynth., Proc. Int. Conf. Photosynth., 8th (1990), Meeting  
Date 1989, Volume 3, 861-3. Editor(s): Baltscheffsky, Margareta.  
Publisher: Kluwer, Dordrecht, Neth.  
CODEN: 57BCAN

DT Conference

LA English

AB The effect of 5° temperature on etioplast-to-chloroplast conversion was  
examined in winter rye upon exposure to intermittent light. The  
5°/intermittent light seedlings developed almost 2-fold higher  
chlorophyll after 48 cycles than did 20° seedlings. Both exhibited  
similar maximum photosystem I activity. Development of photosystem II  
activity was delayed at 5° relative to that observed at 20°.  
Under intermittent light at 20°, a breakdown of prolamellar bodies  
(PB) and a decrease in NADPH-protochlorophyllide oxidoreductase (PCR) was  
observed. In contrast, plastids developed at 5° exhibited PB and  
thylakoid membranes as well as high levels of PCR. The plastid  
transformation from etioplast to chloroplast at low temperature provides an  
excellent opportunity to study more precisely the mechanisms of plastid  
transformation.

TI **Low temperature** effect on **PCR** and  
chlorophyll accumulation in rye seedlings

L5 ANSWER 14 OF 15 MEDLINE on STN

DUPLICATE 4

AN 89078178 MEDLINE

DN PubMed ID: 3203600

TI A programmable system to perform the polymerase chain reaction.

AU Weier H U; Gray J W

CS Biomedical Sciences Division, Lawrence Livermore National Laboratory,  
Livermore, CA.

NC HD17655 (NICHD)

SO DNA (Mary Ann Liebert, Inc.), (1988 Jul-Aug) 7 (6) 441-7.  
Journal code: 8302432. ISSN: 0198-0238.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 198902

ED Entered STN: 19900308

Last Updated on STN: 19980206

Entered Medline: 19890209

AB An automated system is described that performs the cyclic  
**temperature** changes required for enzymatic amplification of  
specific DNA segments in vitro using the polymerase chain reaction (pcr).  
During **pcr**, oligonucleotide primer molecules are bound at

**low temperature** to templates of heat-denatured DNA and extended on their 3' end using a thermostable DNA polymerase. The DNA denaturation, primer annealing, and extension is repeated several times under program control to accumulate a large number of identical copies of the DNA sequence between the primers. A microcomputer system controls the flow of 96 degrees C and 37 degrees C water through a 24-well sample holder so that the **temperature** in the samples in the holder varies as required for DNA denaturation, primer annealing, and DNA polymerization. The microcomputer automatically performs multiple thermal cycles and is sufficiently flexible that the **temperature** profile can be varied from cycle to cycle.

AB An automated system is described that performs the cyclic **temperature** changes required for enzymatic amplification of specific DNA segments in vitro using the polymerase chain reaction (pcr). During **pcr**, oligonucleotide primer molecules are bound at **low temperature** to templates of heat-denatured DNA and extended on their 3' end using a thermostable DNA polymerase. The DNA denaturation, primer. . . controls the flow of 96 degrees C and 37 degrees C water through a 24-well sample holder so that the **temperature** in the samples in the holder varies as required for DNA denaturation, primer annealing, and DNA polymerization. The microcomputer automatically performs multiple thermal cycles and is sufficiently flexible that the **temperature** profile can be varied from cycle to cycle.

L5 ANSWER 15 OF 15 MEDLINE on STN DUPLICATE 5

AN 87241738 MEDLINE

DN PubMed ID: 3593427

TI [ATP-phosphocreatine metabolism catalyzed by creatine kinase. Comparison of saturation transfer (NMR) and isotope labeling technics].  
Izuchenie obmena ATP-fosfokreatin, kataliziruemogo kreatinkinazoi.  
Sravnenie tekhniki perenosy nasyscheniya (IaMR) i metoda izotopnoi metki.  
AU Kupriianov V V; Liulina N V; Shteinshneider A Ia; Zueva M Iu; Saks V A  
SO Bioorganicheskaya khimiya, (1987 Mar) 13 (3) 300-8.  
Journal code: 7804941. ISSN: 0132-3423.

CY USSR

DT Journal; Article; (JOURNAL ARTICLE)

LA Russian

FS Priority Journals

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Last Updated on STN: 19970203

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AB Unidirectional fluxes from ATP to phosphocreatine (PCr) catalyzed by MM-isoenzyme of creatine kinase (CK) were measured by using <sup>31</sup>P-NMR saturation transfer technique and by means of radioactively labeled [gamma-<sup>32</sup>P]ATP. At 30-37 degrees C and pH 7.4 in a wide range of [PCr]/[creatine] ([PCr]/[Cr]) ratios (0.2 to 3.0) both of these methods gave similar results, thus showing that magnetization (saturation) transfer allows to determine fluxes close to real ones under "physiological" conditions. However, at [PCr]/[Cr] ratio higher than 5 ([ADP] less than 30 microm) or at decreased **temperatures** (7-15 degrees C, [PCr]/[Cr] approximately 1) fluxes determined by saturation transfer substantially exceeded those measured with the radioactive label. These data imply that under "physiological" conditions phosphoryl group transfer is actually rate-determining step of the CK reaction. On the contrary, at high [PCr]/[Cr] values or at **low temperature** the control step could be shifted from the phosphoryl group transfer or distributed among other steps of the reaction.

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conditions phosphoryl group transfer is actually rate-determining step of the CK reaction. On the contrary, at high  $[PCr]/[Cr]$  values or at low temperature the control step could be shifted from the phosphoryl group transfer or distributed among other steps of the reaction.

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